

RAW SEQUENCE LISTING

DATE: 05/15/2001

PATENT APPLICATION: US/09/740,288A

TIME: 17:26:37

Input Set : A:\Pto.amc

Output Set: N:\CRF3\05152001\I740288A.raw

PS

3 <110> APPLICANT: Allen, Stephen
 4 Kinney, Anthony
 5 Miao, Guo-Hua
 6 Orozco, Emil
 8 <120> TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
 10 <130> FILE REFERENCE: BB1429 US NA
 12 <140> CURRENT APPLICATION NUMBER: US 09/740288A
 13 <141> CURRENT FILING DATE: 2000-12-19
 15 <150> PRIOR APPLICATION NUMBER: US 60/172929
 16 <151> PRIOR FILING DATE: 1999-12-21
 18 <160> NUMBER OF SEQ ID NOS: 36
 20 <170> SOFTWARE: Microsoft Office 97
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 512
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Hordeum vulgare
 28 <220> FEATURE:
 29 <221> NAME/KEY: Unsure
 30 <222> LOCATION: (94)..(94)
 31 <223> OTHER INFORMATION: n = A, C, G, or T
 34 <220> FEATURE:
 35 <221> NAME/KEY: Unsure
 36 <222> LOCATION: (460)..(460)
 37 <223> OTHER INFORMATION: n = A, C, G, or T
 40 <220> FEATURE:
 41 <221> NAME/KEY: Unsure
 42 <222> LOCATION: (462)..(462)
 43 <223> OTHER INFORMATION: n = A, C, G, or T
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 W-→ 48 ccgagccggc catgatgctg ctgctcgcgc gcancctcgc tcccgcgctc ggtccccctt 120
 49 cgcctccgcc gttagcgccg cgcccttctc atcggtatcg gcggccgcgg cggagggcga 180
 50 cgggcggtgc gggacgggcc caggaacgac tggaccgcgc ccgagatcca ggccatctac 240
 51 gactccccgc tctcgacct cctcttccac gggggtcaag tccataggaa tgtccataaa 300
 52 tttagagaag tgcaacaatg cacacttctt tcaataaaga ctggtgggtg cagcgaagat 360
 53 tgttcatact gcccacagtc ttcaagatac agtaccggat tgaaggctga aaaattaatg 420
 W-→ 54 aagaaagatg ccgtcctaga agcagctaaa aaggcaaagn angctgggag cacccgattt 480
 55 tgattggagc gatggagaga gacaattggc ag 512
 58 <210> SEQ ID NO: 2
 59 <211> LENGTH: 137
 60 <212> TYPE: PRT
 61 <213> ORGANISM: Hordeum vulgare
 63 <220> FEATURE:
 64 <221> NAME/KEY: UNSURE
 65 <222> LOCATION: (131)..(131)
 66 <223> OTHER INFORMATION: Xaa = any amino acid
 69 <400> SEQUENCE: 2

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```

70 Met Met Leu Leu Leu Ala Arg Ser Leu Arg Ser Arg Val Arg Ser Pro
71 1 5 10 15
72 Phe Ala Ser Ala Val Ser Ala Ala Pro Phe Ser Ser Val Ser Ala Ala
73 20 25 30
74 Ala Ala Glu Ala Glu Arg Ala Val Arg Asp Gly Pro Arg Asn Asp Trp
75 35 40 45
76 Thr Arg Pro Glu Ile Gln Ala Ile Tyr Asp Ser Pro Leu Leu Asp Leu
77 50 55 60
78 Leu Phe His Gly Ala Gln Val His Arg Asn Val His Lys Phe Arg Glu
79 65 70 75 80
80 Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu
81 85 90 95
82 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Leu Lys
83 100 105 110
84 Ala Glu Lys Leu Met Lys Lys Asp Ala Val Leu Glu Ala Ala Lys Lys
85 115 120 125

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W-→ 86 Ala Lys Xaa Ala Gly Ser Thr Arg Phe
87 130 135

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90 <210> SEQ ID NO: 3
91 <211> LENGTH: 496
92 <212> TYPE: DNA
93 <213> ORGANISM: Zea mays
95 <220> FEATURE:
96 <221> NAME/KEY: Unsure
97 <222> LOCATION: (33)..(33)
98 <223> OTHER INFORMATION: n = A, C, G, or T
101 <220> FEATURE:
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103 <222> LOCATION: (318)..(318)
104 <223> OTHER INFORMATION: n = A, C, G, or T
107 <220> FEATURE:
108 <221> NAME/KEY: Unsure
109 <222> LOCATION: (321)..(321)
110 <223> OTHER INFORMATION: n = A, C, G, or T
113 <220> FEATURE:
114 <221> NAME/KEY: Unsure
115 <222> LOCATION: (365)..(365)
116 <223> OTHER INFORMATION: n = A, C, G, or T
119 <220> FEATURE:
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121 <222> LOCATION: (446)..(446)
122 <223> OTHER INFORMATION: n = A, C, G, or T
125 <400> SEQUENCE: 3

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W-→ 126 tccaatcggg tgggcagttt ttaaggaaac canggaccgc aagcaagcaa gccgccccag 60
127 ccgacgaggc gaggagcgtg caattccgta gctgcaacga actccctcga ccgtatcgcc 120
128 cgtgctcct ctatcccttt cctgctgctg ctactacctt aagctatcac tatcatggcc 180
129 ttgatgctgc tagcgcgcaa cctgcgctcc cgccctcgcc caccgctcgc cgccgcgcgc 240
130 gggttctcgt cggccgcggc ggaggcggag agggcgatac gggacgggcc gcggaacgac 300
W-→ 131 tggagccggc ccgagatnca ngccgtctac gactcaccgc tcctcgacct cctctttcac 360

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W--> 132 ggggntcagt catcaagata caacactgga ttgaagggcc aaaaattgat gaacaaatat 420
 W--> 133 gctgtcttgg gagcagcaaa aaaggnaaaa gagtctggga agcaaccgtt tttgcatggg 480
 134 aactgcattg gagaaa 496
 137 <210> SEQ ID NO: 4
 138 <211> LENGTH: 102
 139 <212> TYPE: PRT
 140 <213> ORGANISM: Zea mays
 142 <220> FEATURE:
 143 <221> NAME/KEY: UNSURE
 144 <222> LOCATION: (48)..(49)
 145 <223> OTHER INFORMATION: Xaa = any amino acid
 148 <220> FEATURE:
 149 <221> NAME/KEY: UNSURE
 150 <222> LOCATION: (64)..(64)
 151 <223> OTHER INFORMATION: Xaa = any amino acid
 154 <220> FEATURE:
 155 <221> NAME/KEY: UNSURE
 156 <222> LOCATION: (91)..(91)
 157 <223> OTHER INFORMATION: Xaa = any amino acid
 160 <400> SEQUENCE: 4
 161 Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
 162 1 5 10 15
 163 Pro Leu Ala Ala Ala Ala Gly Phe Ser Ser Ala Ala Ala Glu Ala Glu
 164 20 25 30
 W--> 165 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Xaa
 166 35 40 45
 W--> 167 Xaa Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Xaa
 168 50 55 60
 169 Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Gly Gln Lys Leu Met Asn
 170 65 70 75 80
 W--> 171 Lys Tyr Ala Val Leu Gly Ala Ala Lys Lys Xaa Lys Glu Ser Gly Lys
 172 85 90 95
 173 Gln Pro Phe Leu His Gly
 174 100
 177 <210> SEQ ID NO: 5
 178 <211> LENGTH: 497
 179 <212> TYPE: DNA
 180 <213> ORGANISM: Zea mays
 182 <220> FEATURE:
 183 <221> NAME/KEY: Unsure
 184 <222> LOCATION: (192)..(192)
 185 <223> OTHER INFORMATION: n = A, C, G, or T
 188 <220> FEATURE:
 189 <221> NAME/KEY: Unsure
 190 <222> LOCATION: (460)..(460)
 191 <223> OTHER INFORMATION: n = A, C, G, or T
 194 <220> FEATURE:
 195 <221> NAME/KEY: Unsure
 196 <222> LOCATION: (463)..(463)

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197 <223> OTHER INFORMATION: n = A, C, G, or T
 200 <220> FEATURE:
 201 <221> NAME/KEY: Unsure
 202 <222> LOCATION: (469)..(469)
 203 <223> OTHER INFORMATION: n = A, C, G, or T
 206 <220> FEATURE:
 207 <221> NAME/KEY: Unsure
 208 <222> LOCATION: (490)..(490)
 209 <223> OTHER INFORMATION: n = A, C, G, or T
 212 <400> SEQUENCE: 5
 213 agccgacgag gcgaggagcg tgcaattccg tagctgcaac tgcaacgaac tccctccctc 60
 214 cctcgaccgt atcgcccgt gctcctctat ccttttctg ctgctgctac taccttaagc 120
 215 tatcatggcc ttgatgctgc tagcgcgcaa cctgcgctcc cgctccgcc caccgctcgc 180
 W--> 216 cgccgcccgc gngttctcgt cggccgcggc ggagggcgag agggcgatac gggacgggccc 240
 217 gcggaacgac tggagccggc ccgagattca agcgtctac gactcaccgc tccctgacct 300
 218 cctctttcac ggggctcaag tccacagaaa tgtccataaa ttcaagagaa gtgcagcaat 360
 219 gcacacttct ttcaatcaag actggtggga tgcagtgaag attgttctta ctgtcctcaa 420
 W--> 220 gtcatacaag aatacaacac tgggattgaa gggcccaaan aanttgatna acaaaagatg 480
 W--> 221 ctgtcttggg aacaaca 497
 224 <210> SEQ ID NO: 6
 225 <211> LENGTH: 98
 226 <212> TYPE: PRT
 227 <213> ORGANISM: Zea mays
 229 <220> FEATURE:
 230 <221> NAME/KEY: UNSURE
 231 <222> LOCATION: (23)..(23)
 232 <223> OTHER INFORMATION: Xaa = any amino acid
 235 <220> FEATURE:
 236 <221> NAME/KEY: UNSURE
 237 <222> LOCATION: (72)..(72)
 238 <223> OTHER INFORMATION: Xaa = any amino acid
 241 <220> FEATURE:
 242 <221> NAME/KEY: UNSURE
 243 <222> LOCATION: (89)..(89)
 244 <223> OTHER INFORMATION: Xaa = any amino acid
 247 <400> SEQUENCE: 6
 248 Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
 249 1 5 10 15
 OK 250 Pro Leu Ala Ala Ala Ala Xaa Phe Ser Ser Ala Ala Ala Glu Ala Glu
 251 20 25 30
 252 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 253 35 40 45
 254 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 255 50 55 60
 W 256 Gln Val His Arg Asn Val His Xaa Ser Arg Glu Val Gln Gln Cys Thr
 257 65 70 75 80
 W 258 Leu Leu Ser Ile Lys Thr Gly Gly Xaa Ser Glu Asp Cys Ser Tyr Cys
 259 85 90 95
 260 Pro Gln

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264 <210> SEQ ID NO: 7
265 <211> LENGTH: 1152
266 <212> TYPE: DNA
267 <213> ORGANISM: Zea mays
269 <400> SEQUENCE: 7
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271 cgcccgctgc tctctatcc ctttctgtct gctgtacta ccttaagcta tcactatcat      120
272 ggccttgatg ctgctagcgc gcaacctgcg ctcccgctc cgccaccgc tcgccgcccgc      180
273 cgcggcggtc tcgtcgggccg cggcgagggc ggagagggcg atacgggacg ggccgcggaa      240
274 cgactggagc cggcccgaga tccaggccgt ctacgactca ccgctcctcg acctcctctt      300
275 tcacggggct caggtccaca gaaatgtcca taaattcaga gaagtgcagc aatgcacact      360
276 tctttcaatc aagactggtg gatgcagtga agattgttct tactgtctct agtcatcaag      420
277 atacaacact ggattgaagg cccaaaaatt gatgaacaaa tatgtgtctt tggaagcagc      480
278 aaaaaaggca aaagagtctg ggagcaccgc tttttgcatg ggagctgcat ggagagaaac      540
279 cattggcagg aaatcaaact tcaaccagat tcttgaatat gtcaaggaaa taaggggtat      600
280 gggcgtggag gtctgttgca cactaggcat gatagagaaa caacaagctg aagaactcaa      660
281 gaaggctgga cttacagcat ataatcataa cctagatata tcaagagagt attatcccaa      720
282 cattattacc acaagatcat atgatgatag actgcagact cttgagcatg tccgtgaagc      780
283 tggaataagc atctgctcag gtggaatcat tggcttgggt gaagcagagg aggaccgggt      840
284 agggttgttg cataccctag ctaccttgcc tacacacca gagagcgttc ctattaatgc      900
285 attggttgct gtaaaaggca cacctcttga ggaccagaag cctgtagaga tctgggaaat      960
286 gatccgcatg atcgccactg ctgggatcac gatgccaag gcaatggtga ggctttcagc     1020
287 aggcgagta cggttctcga tgccagaaca agcgtgtgct ttctcgtctg gggccaactc     1080
288 catccttgcc ggcgagaaac ttctcacaac cgcaacaac gactttgatg cggaccaagc     1140
289 gatgttcaag at                                     1152
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293 <211> LENGTH: 344
294 <212> TYPE: PRT
295 <213> ORGANISM: Zea mays
297 <400> SEQUENCE: 8
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299 1 5 10 15
300 Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
301 20 25 30
302 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
303 35 40 45
304 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
305 50 55 60
306 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
307 65 70 75 80
308 Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
309 85 90 95
310 Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
311 100 105 110
312 Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
313 115 120 125
314 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
315 130 135 140
316 Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly

```

Please Note:

Use f n and/or Xaa have been detected in the Sequence Listing. Pl as revi w the Sequence Listing to ensure that a corresp nding explanation is presented in the <220> to <223> fields of each sequence which presents at least ne n or Xaa.

VERIFICATION SUMMARY

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L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
 L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
 L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
 L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
 L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
 L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
 L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
 L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
 L:1517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36